



IFWO

RAW SEQUENCE LISTING

DATE: 08/27/2004

PATENT APPLICATION: US/10/728,696

TIME: 11:50:30

Input Set : N:\Crf3\RULE60\10728696.raw

Output Set: N:\CRF4\08272004\J728696.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Williams, James A.

6 Thalley, Bruce S.

8 (ii) TITLE OF INVENTION: Multivalent Vaccine For Clostridium

9 Botulinum Neurotoxin

11 (iii) NUMBER OF SEQUENCES: 82

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Medlen & Carroll

15 (B) STREET: 220 Montgomery Street, Suite 2200

16 (C) CITY: San Francisco

17 (D) STATE: California

18 (E) COUNTRY: United States of America

19 (F) ZIP: 94104

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

28 (A) APPLICATION NUMBER: US/10/728,696

29 (B) FILING DATE: 05-Dec-2003

30 (C) CLASSIFICATION: 424

31 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: US/08/704,159

33 (B) FILING DATE: 28-AUG-1996

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Ingolia, Diane E.

36 (B) REGISTRATION NUMBER: 40,027

37 (C) REFERENCE/DOCKET NUMBER: OPHD-02304

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: (415) 705-8410

41 (B) TELEFAX: (415) 397-8338

44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:

47 (A) LENGTH: 24 base pairs

48 (B) TYPE: nucleic acid

49 (C) STRANDEDNESS: single

50 (D) TOPOLOGY: linear

52 (ii) MOLECULE TYPE: DNA (genomic)

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

58 GGAAATTTAG CTGCAGCATC TGAC

60 (2) INFORMATION FOR SEQ ID NO: 2:

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24

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62      (i) SEQUENCE CHARACTERISTICS:
63          (A) LENGTH: 24 base pairs
64          (B) TYPE: nucleic acid
65          (C) STRANDEDNESS: single
66          (D) TOPOLOGY: linear
68      (ii) MOLECULE TYPE: DNA (genomic)
72      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
74 TCTAGCAAAT TCGCTTGTGT TGAA                                     24
76 (2) INFORMATION FOR SEQ ID NO: 3:
78      (i) SEQUENCE CHARACTERISTICS:
79          (A) LENGTH: 20 base pairs
80          (B) TYPE: nucleic acid
81          (C) STRANDEDNESS: single
82          (D) TOPOLOGY: linear
84      (ii) MOLECULE TYPE: DNA (genomic)
88      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
90 CTCGCATATA GCATTAGACC                                         20
92 (2) INFORMATION FOR SEQ ID NO: 4:
94      (i) SEQUENCE CHARACTERISTICS:
95          (A) LENGTH: 19 base pairs
96          (B) TYPE: nucleic acid
97          (C) STRANDEDNESS: single
98          (D) TOPOLOGY: linear
100     (ii) MOLECULE TYPE: DNA (genomic)
104     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
106 CTATCTAGGC CTAAAGTAT                                         19
108 (2) INFORMATION FOR SEQ ID NO: 5:
110     (i) SEQUENCE CHARACTERISTICS:
111         (A) LENGTH: 8133 base pairs
112         (B) TYPE: nucleic acid
113         (C) STRANDEDNESS: single
114         (D) TOPOLOGY: linear
116     (ii) MOLECULE TYPE: DNA (genomic)
119     (ix) FEATURE:
120         (A) NAME/KEY: CDS
121         (B) LOCATION: 1..8130
124     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
126 ATG TCT TTA ATA TCT AAA GAA GAG TTA ATA AAA CTC GCA TAT AGC ATT       48
127 Met Ser Leu Ile Ser Lys Glu Glu Leu Ile Lys Leu Ala Tyr Ser Ile
128 1      5      10      15
130 AGA CCA AGA GAA AAT GAG TAT AAA ACT ATA CTA ACT AAT TTA GAC GAA       96
131 Arg Pro Arg Glu Asn Glu Tyr Lys Thr Ile Leu Thr Asn Leu Asp Glu
132      20      25      30
134 TAT AAT AAG TTA ACT ACA AAC AAT AAT GAA AAT AAA TAT TTG CAA TTA      144
135 Tyr Asn Lys Leu Thr Thr Asn Asn Asn Glu Asn Lys Tyr Leu Gln Leu
136      35      40      45
138 AAA AAA CTA AAT GAA TCA ATT GAT GTT TTT ATG AAT AAA TAT AAA ACT      192
139 Lys Lys Leu Asn Glu Ser Ile Asp Val Phe Met Asn Lys Tyr Lys Thr
140      50      55      60

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142	TCA	AGC	AGA	AAT	AGA	GCA	CTC	TCT	AAT	CTA	AAA	AAA	GAT	ATA	TTA	AAA	240
143	Ser	Ser	Arg	Asn	Arg	Ala	Leu	Ser	Asn	Leu	Lys	Lys	Asp	Ile	Leu	Lys	
144	65					70					75					80	
146	GAA	GTA	ATT	CTT	ATT	AAA	AAT	TCC	AAT	ACA	AGC	CCT	GTA	GAA	AAA	AAT	288
147	Glu	Val	Ile	Leu	Ile	Lys	Asn	Ser	Asn	Thr	Ser	Pro	Val	Glu	Lys	Asn	
148					85					90					95		
150	TTA	CAT	TTT	GTA	TGG	ATA	GGT	GGA	GAA	GTC	AGT	GAT	ATT	GCT	CTT	GAA	336
151	Leu	His	Phe	Val	Trp	Ile	Gly	Gly	Glu	Val	Ser	Asp	Ile	Ala	Leu	Glu	
152				100					105				110				
154	TAC	ATA	AAA	CAA	TGG	GCT	GAT	ATT	AAT	GCA	GAA	TAT	AAT	ATT	AAA	CTG	384
155	Tyr	Ile	Lys	Gln	Trp	Ala	Asp	Ile	Asn	Ala	Glu	Tyr	Asn	Ile	Lys	Leu	
156			115					120					125				
158	TGG	TAT	GAT	AGT	GAA	GCA	TTC	TTA	GTA	AAT	ACA	CTA	AAA	AAG	GCT	ATA	432
159	Trp	Tyr	Asp	Ser	Glu	Ala	Phe	Leu	Val	Asn	Thr	Leu	Lys	Lys	Ala	Ile	
160		130					135					140					
162	GTT	GAA	TCT	TCT	ACC	ACT	GAA	GCA	TTA	CAG	CTA	CTA	GAG	GAA	GAG	ATT	480
163	Val	Glu	Ser	Ser	Thr	Thr	Glu	Ala	Leu	Gln	Leu	Leu	Glu	Glu	Glu	Ile	
164	145				150					155					160		
166	CAA	AAT	CCT	CAA	TTT	GAT	AAT	ATG	AAA	TTT	TAC	AAA	AAA	AGG	ATG	GAA	528
167	Gln	Asn	Pro	Gln	Phe	Asp	Asn	Met	Lys	Phe	Tyr	Lys	Lys	Arg	Met	Glu	
168				165						170				175			
170	TTT	ATA	TAT	GAT	AGA	CAA	AAA	AGG	TTT	ATA	AAT	TAT	TAT	AAA	TCT	CAA	576
171	Phe	Ile	Tyr	Asp	Arg	Gln	Lys	Arg	Phe	Ile	Asn	Tyr	Tyr	Lys	Ser	Gln	
172				180					185					190			
174	ATC	AAT	AAA	CCT	ACA	GTA	CCT	ACA	ATA	GAT	GAT	ATT	ATA	AAG	TCT	CAT	624
175	Ile	Asn	Lys	Pro	Thr	Val	Pro	Thr	Ile	Asp	Asp	Ile	Ile	Lys	Ser	His	
176			195					200					205				
178	CTA	GTA	TCT	GAA	TAT	AAT	AGA	GAT	GAA	ACT	GTA	TTA	GAA	TCA	TAT	AGA	672
179	Leu	Val	Ser	Glu	Tyr	Asn	Arg	Asp	Glu	Thr	Val	Leu	Glu	Ser	Tyr	Arg	
180		210					215						220				
182	ACA	AAT	TCT	TTG	AGA	AAA	ATA	AAT	AGT	AAT	CAT	GGG	ATA	GAT	ATC	AGG	720
183	Thr	Asn	Ser	Leu	Arg	Lys	Ile	Asn	Ser	Asn	His	Gly	Ile	Asp	Ile	Arg	
184	225				230					235					240		
186	GCT	AAT	AGT	TTG	TTT	ACA	GAA	CAA	GAG	TTA	TTA	AAT	ATT	TAT	AGT	CAG	768
187	Ala	Asn	Ser	Leu	Phe	Thr	Glu	Gln	Glu	Leu	Leu	Asn	Ile	Tyr	Ser	Gln	
188				245						250				255			
190	GAG	TTG	TTA	AAT	CGT	GGA	AAT	TTA	GCT	GCA	GCA	TCT	GAC	ATA	GTA	AGA	816
191	Glu	Leu	Leu	Asn	Arg	Gly	Asn	Leu	Ala	Ala	Ala	Ser	Asp	Ile	Val	Arg	
192				260					265					270			
194	TTA	TTA	GCC	CTA	AAA	AAT	TTT	GGC	GGA	GTA	TAT	TTA	GAT	GTT	GAT	ATG	864
195	Leu	Leu	Ala	Leu	Lys	Asn	Phe	Gly	Gly	Val	Tyr	Leu	Asp	Val	Asp	Met	
196			275					280					285				
198	CTT	CCA	GGT	ATT	CAC	TCT	GAT	TTA	TTT	AAA	ACA	ATA	TCT	AGA	CCT	AGC	912
199	Leu	Pro	Gly	Ile	His	Ser	Asp	Leu	Phe	Lys	Thr	Ile	Ser	Arg	Pro	Ser	
200		290					295					300					
202	TCT	ATT	GGA	CTA	GAC	CGT	TGG	GAA	ATG	ATA	AAA	TTA	GAG	GCT	ATT	ATG	960
203	Ser	Ile	Gly	Leu	Asp	Arg	Trp	Glu	Met	Ile	Lys	Leu	Glu	Ala	Ile	Met	
204	305				310						315				320		
206	AAG	TAT	AAA	AAA	TAT	ATA	AAT	AAT	TAT	ACA	TCA	GAA	AAC	TTT	GAT	AAA	1008

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207	Lys	Tyr	Lys	Lys	Tyr	Ile	Asn	Asn	Tyr	Thr	Ser	Glu	Asn	Phe	Asp	Lys	
208					325					330					335		
210	CTT	GAT	CAA	CAA	TTA	AAA	GAT	AAT	TTT	AAA	CTC	ATT	ATA	GAA	AGT	AAA	1056
211	Leu	Asp	Gln	Gln	Leu	Lys	Asp	Asn	Phe	Lys	Leu	Ile	Ile	Glu	Ser	Lys	
212				340					345					350			
214	AGT	GAA	AAA	TCT	GAG	ATA	TTT	TCT	AAA	TTA	GAA	AAT	TTA	AAT	GTA	TCT	1104
215	Ser	Glu	Lys	Ser	Glu	Ile	Phe	Ser	Lys	Leu	Glu	Asn	Leu	Asn	Val	Ser	
216			355					360					365				
218	GAT	CTT	GAA	ATT	AAA	ATA	GCT	TTC	GCT	TTA	GGC	AGT	GTT	ATA	AAT	CAA	1152
219	Asp	Leu	Glu	Ile	Lys	Ile	Ala	Phe	Ala	Leu	Gly	Ser	Val	Ile	Asn	Gln	
220		370					375					380					
222	GCC	TTG	ATA	TCA	AAA	CAA	GGT	TCA	TAT	CTT	ACT	AAC	CTA	GTA	ATA	GAA	1200
223	Ala	Leu	Ile	Ser	Lys	Gln	Gly	Ser	Tyr	Leu	Thr	Asn	Leu	Val	Ile	Glu	
224	385				390					395					400		
226	CAA	GTA	AAA	AAT	AGA	TAT	CAA	TTT	TTA	AAC	CAA	CAC	CTT	AAC	CCA	GCC	1248
227	Gln	Val	Lys	Asn	Arg	Tyr	Gln	Phe	Leu	Asn	Gln	His	Leu	Asn	Pro	Ala	
228				405					410				415				
230	ATA	GAG	TCT	GAT	AAT	AAC	TTC	ACA	GAT	ACT	ACT	AAA	ATT	TTT	CAT	GAT	1296
231	Ile	Glu	Ser	Asp	Asn	Asn	Phe	Thr	Asp	Thr	Thr	Lys	Ile	Phe	His	Asp	
232			420						425				430				
234	TCA	TTA	TTT	AAT	TCA	GCT	ACC	GCA	GAA	AAC	TCT	ATG	TTT	TTA	ACA	AAA	1344
235	Ser	Leu	Phe	Asn	Ser	Ala	Thr	Ala	Glu	Asn	Ser	Met	Phe	Leu	Thr	Lys	
236			435					440				445					
238	ATA	GCA	CCA	TAC	TTA	CAA	GTA	GGT	TTT	ATG	CCA	GAA	GCT	CGC	TCC	ACA	1392
239	Ile	Ala	Pro	Tyr	Leu	Gln	Val	Gly	Phe	Met	Pro	Glu	Ala	Arg	Ser	Thr	
240		450					455					460					
242	ATA	AGT	TTA	AGT	GGT	CCA	GGA	GCT	TAT	GCG	TCA	GCT	TAC	TAT	GAT	TTC	1440
243	Ile	Ser	Leu	Ser	Gly	Pro	Gly	Ala	Tyr	Ala	Ser	Ala	Tyr	Tyr	Asp	Phe	
244	465				470					475					480		
246	ATA	AAT	TTA	CAA	GAA	AAT	ACT	ATA	GAA	AAA	ACT	TTA	AAA	GCA	TCA	GAT	1488
247	Ile	Asn	Leu	Gln	Glu	Asn	Thr	Ile	Glu	Lys	Thr	Leu	Lys	Ala	Ser	Asp	
248				485					490				495				
250	TTA	ATA	GAA	TTT	AAA	TTC	CCA	GAA	AAT	AAT	CTA	TCT	CAA	TTG	ACA	GAA	1536
251	Leu	Ile	Glu	Phe	Lys	Phe	Pro	Glu	Asn	Asn	Leu	Ser	Gln	Leu	Thr	Glu	
252			500						505				510				
254	CAA	GAA	ATA	AAT	AGT	CTA	TGG	AGC	TTT	GAT	CAA	GCA	AGT	GCA	AAA	TAT	1584
255	Gln	Glu	Ile	Asn	Ser	Leu	Trp	Ser	Phe	Asp	Gln	Ala	Ser	Ala	Lys	Tyr	
256			515					520				525					
258	CAA	TTT	GAG	AAA	TAT	GTA	AGA	GAT	TAT	ACT	GGT	GGA	TCT	CTT	TCT	GAA	1632
259	Gln	Phe	Glu	Lys	Tyr	Val	Arg	Asp	Tyr	Thr	Gly	Gly	Ser	Leu	Ser	Glu	
260		530					535					540					
262	GAC	AAT	GGG	GTA	GAC	TTT	AAT	AAA	AAT	ACT	GCC	CTC	GAC	AAA	AAC	TAT	1680
263	Asp	Asn	Gly	Val	Asp	Phe	Asn	Lys	Asn	Thr	Ala	Leu	Asp	Lys	Asn	Tyr	
264	545				550					555					560		
266	TTA	TTA	AAT	AAT	AAA	ATT	CCA	TCA	AAC	AAT	GTA	GAA	GAA	GCT	GGA	AGT	1728
267	Leu	Leu	Asn	Asn	Lys	Ile	Pro	Ser	Asn	Asn	Val	Glu	Glu	Ala	Gly	Ser	
268				565					570				575				
270	AAA	AAT	TAT	GTT	CAT	TAT	ATC	ATA	CAG	TTA	CAA	GGA	GAT	GAT	ATA	AGT	1776
271	Lys	Asn	Tyr	Val	His	Tyr	Ile	Ile	Gln	Leu	Gln	Gly	Asp	Asp	Ile	Ser	

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272	580	585	590	
274	TAT GAA GCA ACA TGC AAT TTA TTT TCT AAA AAT CCT AAA AAT AGT ATT	1824		
275	Tyr Glu Ala Thr Cys Asn Leu Phe Ser Lys Asn Pro Lys Asn Ser Ile			
276	595 600 605			
278	ATT ATA CAA CGA AAT ATG AAT GAA AGT GCA AAA AGC TAC TTT TTA AGT	1872		
279	Ile Ile Gln Arg Asn Met Asn Glu Ser Ala Lys Ser Tyr Phe Leu Ser			
280	610 615 620			
282	GAT GAT GGA GAA TCT ATT TTA GAA TTA AAT AAA TAT AGG ATA CCT GAA	1920		
283	Asp Asp Gly Glu Ser Ile Leu Glu Leu Asn Lys Tyr Arg Ile Pro Glu			
284	625 630 635 640			
286	AGA TTA AAA AAT AAG GAA AAA GTA AAA GTA ACC TTT ATT GGA CAT GGT	1968		
287	Arg Leu Lys Asn Lys Glu Lys Val Lys Val Thr Phe Ile Gly His Gly			
288	645 650 655			
290	AAA GAT GAA TTC AAC ACA AGC GAA TTT GCT AGA TTA AGT GTA GAT TCA	2016		
291	Lys Asp Glu Phe Asn Thr Ser Glu Phe Ala Arg Leu Ser Val Asp Ser			
292	660 665 670			
294	CTT TCC AAT GAG ATA AGT TCA TTT TTA GAT ACC ATA AAA TTA GAT ATA	2064		
295	Leu Ser Asn Glu Ile Ser Ser Phe Leu Asp Thr Ile Lys Leu Asp Ile			
296	675 680 685			
298	TCA CCT AAA AAT GTA GAA GTA AAC TTA CTT GGA TGT AAT ATG TTT AGT	2112		
299	Ser Pro Lys Asn Val Glu Val Asn Leu Leu Gly Cys Asn Met Phe Ser			
300	690 695 700			
302	TAT GAT TTT AAT GTT GAA GAA ACT TAT CCT GGG AAG TTG CTA TTA AGT	2160		
303	Tyr Asp Phe Asn Val Glu Glu Thr Tyr Pro Gly Lys Leu Leu Leu Ser			
304	705 710 715 720			
306	ATT ATG GAC AAA ATT ACT TCC ACT TTA CCT GAT GTA AAT AAA AAT TCT	2208		
307	Ile Met Asp Lys Ile Thr Ser Thr Leu Pro Asp Val Asn Lys Asn Ser			
308	725 730 735			
310	ATT ACT ATA GGA GCA AAT CAA TAT GAA GTA AGA ATT AAT AGT GAG GGA	2256		
311	Ile Thr Ile Gly Ala Asn Gln Tyr Glu Val Arg Ile Asn Ser Glu Gly			
312	740 745 750			
314	AGA AAA GAA CTT CTG GCT CAC TCA GGT AAA TGG ATA AAT AAA GAA GAA	2304		
315	Arg Lys Glu Leu Leu Ala His Ser Gly Lys Trp Ile Asn Lys Glu Glu			
316	755 760 765			
318	GCT ATT ATG AGC GAT TTA TCT AGT AAA GAA TAC ATT TTT TTT GAT TCT	2352		
319	Ala Ile Met Ser Asp Leu Ser Ser Lys Glu Tyr Ile Phe Phe Asp Ser			
320	770 775 780			
322	ATA GAT AAT AAG CTA AAA GCA AAG TCC AAG AAT ATT CCA GGA TTA GCA	2400		
323	Ile Asp Asn Lys Leu Lys Ala Lys Ser Lys Asn Ile Pro Gly Leu Ala			
324	785 790 795 800			
326	TCA ATA TCA GAA GAT ATA AAA ACA TTA TTA CTT GAT GCA AGT GTT AGT	2448		
327	Ser Ile Ser Glu Asp Ile Lys Thr Leu Leu Leu Asp Ala Ser Val Ser			
328	805 810 815			
330	CCT GAT ACA AAA TTT ATT TTA AAT AAT CTT AAG CTT AAT ATT GAA TCT	2496		
331	Pro Asp Thr Lys Phe Ile Leu Asn Asn Leu Lys Leu Asn Ile Glu Ser			
332	820 825 830			
334	TCT ATT GGG GAT TAC ATT TAT TAT GAA AAA TTA GAG CCT GTT AAA AAT	2544		
335	Ser Ile Gly Asp Tyr Ile Tyr Tyr Glu Lys Leu Glu Pro Val Lys Asn			
336	835 840 845			

VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:4168 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=32
L:11352 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=82